

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/620256

Source: IFW

Date Processed by STIC: 12/3/4

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/03/2004

PATENT APPLICATION: US/10/620,256

TIME: 12:32:51

Input Set : N:\Crf3\RULE60\10620256.raw

Output Set: N:\CRF4\12032004\J620256.raw

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1 <110> APPLICANT: Conneely, Orla M
2   Headon, Denis R.
3   O'Malley, Bert W.
4   May, Gregory S.
5 <120> TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
6   AND LACTOFERRIN POLYPEPTIDES USING cDNA SEQUENCES IN VARIOUS
7   ORGANISMS
8 <130> FILE REFERENCE: 01380023US02
9 <140> CURRENT APPLICATION NUMBER: US/10/620,256
10 <141> CURRENT FILING DATE: 2003-07-15
11 <150> PRIOR APPLICATION NUMBER: US/09/633,739
12 <151> PRIOR FILING DATE: 2000-08-07
13 <150> PRIOR APPLICATION NUMBER: 08/456,108
14 <151> PRIOR FILING DATE: 1995-05-30
15 <160> NUMBER OF SEQ ID NOS: 14
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2360
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
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25   aggccacaaa atgcttccaa tggcaaagga atatgagaag agtgcggtggc cctcctgtca      180
26   gctgcataaa gagagactcc cccatccagt gtatccaggc cattgcggaa aacagggccg      240
27   atgctgtgac ccttgatggt ggtttcatat acgaggcagg cctggccccc tacaaactgc      300
28   gacctgtagc ggcggaagtc tacgggaccg aaagacagcc acgaactcac tattatgccg      360
29   tggtgtgtgt gaagaagggc ggcagctttc agctgaacga actgcaaggt ctgaagtcct      420
30   gccacacagg ccttcgcagg accgctggat ggaatgtgcc tatagggaca cttcgtccat      480
31   tcttgaattg gacgggtcca cctgagccca ttgaggcagc tgtggccagg ttcttctcag      540
32   ccagctgtgt tcccggtgca gataaaggac agttcccca cctgtgtcgc ctgtgtgagg      600
33   ggacagggga aaacaaatgt gccttctcct cccaggaacc gtacttcagc tactctggtg      660
34   ccttcaagtg tctgagagac ggggctggag acgtggcttt tatcagagag agcacagtgt      720
35   ttgaggacct gtcagacgag gctgaaaggg acgagtatga gttactctgc ccagacaaca      780
36   ctcggaagcc agtggacaag ttcaaagact gccatctggc cggggtccct tctcatgccg      840
37   ttgtggcacg aagtgtgaat ggcaaggagg atgccatctg gaatcttctc cgccaggcac      900
38   aggaaaagtt tggaaaggac aagtcaccga aattccagct ctttggctcc cctagtgggc      960
39   agaaagatct gctgttcaag gactctgcc a ttgggttttc gaggggtgcc ccgaggatag      1020
40   attctgggct gtaccttggc tccggctact tctactgcat ccagaacttg aggaaaagtg      1080
41   aggaggaagt ggctgcccgg cgtgcgcggg tctgtgtggt tgcgggtggg gagcaggagc      1140
42   tgcgcaagtg taaccagtgg agtggcttga gcgaaggcag cgtgacctgc tcctcgccct      1200
43   ccaccacaga ggactgcac gccctgggtgc tgaaaggaga agctgatgcc atgagtttgg      1260
44   atggaggata tgtgtacact gcaggcaaat gtggtttggt gcctgtcctg gcagagaact      1320

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45      acaaatccca acaaagcagt gaccctgata ctaactgtgt ggatagacct gtggaaggat      1380
46      atcttgctgt ggcggtggtt aggagatcag aactagacct tacctggaac tctgtgaaag      1440
47      gcaagaagtc ctgccacacc gccgtggaca ggactgcagg ctggaatatc cccatgggcc      1500
48      tgctcttcaa ccagacgggc tcctgcaaat ttgatgaata tttcagtcaa agctgtgccc      1560
49      ctgggtctga cccgagatct aatctctgtg ctctgtgtat tggcgacgag cagggtgaga      1620
50      ataagtgcgt gcccaacagc aatgagagat actacggcta cactggggct ttccggtgcc      1680
51      tggctgagaa tgctggagac gttgcatttg tgaaagatgt cactgtcttg cagaacactg      1740
52      atggaaataa caatgaggca tgggctaagg atttgaagct ggcagacttt gcgctgctgt      1800
53      gctcgtatgg caaacggaag cctgtgactg aggcctagaag ctgccatctt gccatggccc      1860
54      cgaatcatgc cgtggtgtct cggatggata aggtggaacg cctgaaacag gtgctgctcc      1920
55      accaacaggc taaatttggg agaaatggat ctgactgccc ggacaagtgt tgcttattcc      1980
56      agtctgaaac caaaaacctt ctgttcaatg acaacactga gtgtctggcc agactccatg      2040
57      gcaaaacaac atatgaaaaa tatttgggac cacagtatgt cgcaggcatt actaatctga      2100
58      aaaagtgtct aacctcccc ctctggaag cctgtgaatt cctcaggaag taaaaccgaa      2160
59      gaagatggcc cagctcccca agaaagcctc agccattcac tggccccagc tcttctcccc      2220
60      aggtgtgttg gggccttggc tcccctgctg aaggtgggga ttgcccattc atctgcttac      2280
61      aattccctgc tgtcgtctta gcaagaagta aatgagaaa tttgtttgaa aaaaaaaaaa      2340
62      aaaaaaaaaa aaaaaaaaaa                                2360

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64 <210> SEQ ID NO: 2

65 <211> LENGTH: 711

66 <212> TYPE: PRT

67 <213> ORGANISM: Homo sapiens

68 <400> SEQUENCE: 2

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69      Met Lys Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu
70      1          5          10          15
71      Cys Leu Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Thr Val Ser
72      20          25          30
73      Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Arg
74      35          40          45
75      Val Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln
76      50          55          60
77      Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp
78      65          70          75          80
79      Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro
80      85          90          95
81      Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr
82      100         105         110
83      Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu
84      115         120         125
85      Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly
86      130         135         140
87      Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly
88      145         150         155         160
89      Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser
90      165         170         175
91      Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu
92      180         185         190
93      Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro
94      195         200         205

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95   Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly
96       210                215                220
97   Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp
98       225                230                235                240
99   Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg
100              245                250                255
101   Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser
102              260                265                270
103   His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp
104              275                280                285
105   Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro
106              290                295                300
107   Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe
108       305                310                315                320
109   Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser
110              325                330                335
111   Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg
112              340                345                350
113   Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys
114              355                360                365
115   Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu
116       370                375                380
117   Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys
118       385                390                395                400
119   Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly
120              405                410                415
121   Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala
122              420                425                430
123   Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val
124              435                440                445
125   Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser
126       450                455                460
127   Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His
128       465                470                475                480
129   Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu
130              485                490                495
131   Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser
132              500                505                510
133   Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile
134              515                520                525
135   Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg
136       530                535                540
137   Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly
138       545                550                555                560
139   Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly
140              565                570                575
141   Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala
142              580                585                590
143   Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser

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Input Set : N:\Crif3\RULE60\10620256.raw

Output Set : N:\CRF4\12032004\J620256.raw

144		595		600		605	
145	Cys	His	Leu	Ala	Met	Ala	Pro
146		610		615		620	
147	Lys	Val	Glu	Arg	Leu	Lys	Gln
148		625		630		635	
149	Gly	Arg	Asn	Gly	Ser	Asp	Cys
150			645		650		655
151	Glu	Thr	Lys	Asn	Leu	Leu	Phe
152			660		665		670
153	Leu	His	Gly	Lys	Thr	Thr	Tyr
154			675		680		685
155	Ala	Gly	Ile	Thr	Asn	Leu	Lys
156			690		695		700
157	Ala	Cys	Glu	Phe	Leu	Arg	Lys
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160 <210> SEQ ID NO: 3
 161 <211> LENGTH: 2347
 162 <212> TYPE: DNA
 163 <213> ORGANISM: Bos taurus
 164 <400> SEQUENCE: 3

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166	cctgtccctt	ggagcccttg	gactgtgtct	ggctgccccg	aggaaaaacg	ttcgatgggtg	120
167	taccatctcc	caacctgagt	ggttcaaattg	ccgcagatgg	cagtggagga	tgaagaagct	180
168	gggtgctccc	tctatcacct	gtgtgaggcg	ggcctttgcc	ttggaatgta	ttccgggcat	240
169	cgcgagaaaa	aaggcggatg	ctgtgacct	ggatgggtggc	atgggtgttg	aggcggggccg	300
170	ggacccctac	aaactgcggc	cagtagcagc	agagatctat	gggacgaaag	agtctcccca	360
171	aacccactat	tatgctgtgg	ccgtcgtgaa	gaagggcagc	aactttcagc	tggaccagct	420
172	gcaaggccgg	aagtccctgc	atacgggcct	tggcaggtcc	gctgggtgga	tcatccctat	480
173	gggaatcctt	cgcccgtact	tgagctggac	agagtcactc	gagccctcc	aggagctgt	540
174	ggctaaattc	ttctctgcca	gctgtgttcc	ctgcattgat	agacaagcat	accccaacct	600
175	gtgtcaactg	tgcaaggggg	agggggagaa	ccagtgtgcc	tgctcctccc	gggaaccata	660
176	cttcggttat	tctggtgcct	tcaagtgtct	gcaggacggg	gctggagacg	tggcttttgt	720
177	taaagagacg	acagtgtttg	agaacttgcc	agagaaggct	gacagggacc	agtatgagct	780
178	tctctgcctg	aacaacagtc	gggcgccagt	ggatgcgttc	aaggagtgcc	acctggccca	840
179	ggtcccttct	catgctgtcg	tggcccgaag	tgtggatggc	aaggaagact	tgatctggaa	900
180	gcttctcagc	aaggcgcagg	agaaatctgg	aaaaaacaag	tctcggagct	tccagctctt	960
181	tggctctcca	cccgcccaga	gggacctgct	gttcaaagac	tctgctcttg	ggtttttgag	1020
182	gatccctcgc	aaggtagatt	cggcgctgta	cctgggctcc	cgctacttga	ccaccttgaa	1080
183	gaacctcagg	gaaactgcgg	aggaggtgaa	ggcgcgttac	accagggtcg	tgtggtgtgc	1140
184	cgtgggacct	gaggagcaga	agaagtgcc	gcagtggagc	cagcagagcg	gccagaacgt	1200
185	gacctgtgcc	acggcgtcca	ccactgacga	ctgcacgtc	ctggtgctga	aaggggaagc	1260
186	agatgccctg	aacttggtatg	gaggatatat	ctacactgcg	ggcaagtgtg	gcctggtgcc	1320
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189	ttctctgaaa	gacaagaagt	cgtgccacac	cgccgtggac	aggactgcag	gctggaacat	1500
190	ccccatgggc	ctgatcgtca	accagacagg	ctcctgcgca	tttgatgaat	tcttttagtca	1560
191	gagctgtgcc	cctggggctg	acccgaaatc	cagactctgt	gccttgtgtg	ctggcgatga	1620
192	ccagggcctg	gacaagtgtg	tgcccaactc	taaggagaag	tactatggct	ataccggggc	1680
193	tttcaggtgc	ctggctgagg	acgttgggga	cgttgccttt	gtgaaaaacg	acacagtctg	1740

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194 ggagaacacg aatggagaga gcactgcaga ctgggctaag aacttgaatc gtgaggactt 1800
195 caggttgctc tgccctcgatg gcaccaggaa gcctgtgacg gaggctcaga gctgccacct 1860
196 ggcggtggcc ccgaatcacg ctgtggtgtc tcggagcgat agggcagcac acgtgaaaca 1920
197 ggtgctgctc caccagcagg ctctgttttg gaaaaatgga aaaaactgcc cggacaagtt 1980
198 ttgtttgttc aaatctgaaa ccaaaaacct tctgttcaat gacaacactg agtgtctggc 2040
199 caaacttgga ggcagaccaa cgtatgaaga atatttgggg acagagtatg tcacggccat 2100
200 tgccaacctg aaaaaatgct caacctcccc gcttctggaa gcctgcgcct tcctgacgag 2160
201 gtaaagcctg caaagaagct agcctgcctc cctgggcctc agctcctccc tgctctcagc 2220
202 cccaatctcc aggcgcgagg gaccttcctc tcccttcctg aagtcggatt tttgccaagc 2280
203 tcatcagtat ttacaattcc ctgctgtcat tttagcaaga aataaaatta gaaatgctgt 2340
204 tgaaaaa 2347
206 <210> SEQ ID NO: 4
207 <211> LENGTH: 708
208 <212> TYPE: PRT
209 <213> ORGANISM: Bos taurus
210 <400> SEQUENCE: 4
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214 20 25 30
215 Pro Glu Trp Phe Lys Cys Arg Arg Trp Gln Trp Arg Met Lys Lys Leu
216 35 40 45
217 Gly Ala Pro Ser Ile Thr Cys Val Arg Arg Ala Phe Ala Leu Glu Cys
218 50 55 60
219 Ile Pro Gly Ile Ala Glu Lys Lys Ala Asp Ala Val Thr Leu Asp Gly
220 65 70 75 80
221 Gly Met Val Phe Glu Ala Gly Arg Asp Pro Tyr Lys Leu Arg Pro Val
222 85 90 95
223 Ala Ala Glu Ile Tyr Gly Thr Lys Glu Ser Pro Gln Thr His Tyr Tyr
224 100 105 110
225 Ala Val Ala Val Val Lys Lys Gly Ser Asn Phe Gln Leu Asp Gln Leu
226 115 120 125
227 Gln Gly Arg Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp
228 130 135 140
229 Ile Ile Pro Met Gly Ile Leu Arg Pro Tyr Leu Ser Trp Thr Glu Ser
230 145 150 155 160
231 Leu Glu Pro Leu Gln Gly Ala Val Ala Lys Phe Phe Ser Ala Ser Cys
232 165 170 175
233 Val Pro Cys Ile Asp Arg Gln Ala Tyr Pro Asn Leu Cys Gln Leu Cys
234 180 185 190
235 Lys Gly Glu Gly Glu Asn Gln Cys Ala Cys Ser Ser Arg Glu Pro Tyr
236 195 200 205
237 Phe Gly Tyr Ser Gly Ala Phe Lys Cys Leu Gln Asp Gly Ala Gly Asp
238 210 215 220
239 Val Ala Phe Val Lys Glu Thr Thr Val Phe Glu Asn Leu Pro Glu Lys
240 225 230 235 240
241 Ala Asp Arg Asp Gln Tyr Glu Leu Leu Cys Leu Asn Asn Ser Arg Ala
242 245 250 255
243 Pro Val Asp Ala Phe Lys Glu Cys His Leu Ala Gln Val Pro Ser His

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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VERIFICATION SUMMARY

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